

# BEST AVAILABLE COPY

1 tGCCTATCTCCCTTTGCCAGGGGGCAGAGAAATGATGgagGTGAATAGCACTTGCTTGA  
-----+-----+-----+-----+ 60  
aCGGATAGAGGGAAACGGTCCCCCGTCTCTTTACTACctcCACTTATCGTGAACGAACCT

b M H E V N S T C L D -

61 TTGCAGGACACCTGGTACCATACGAACAGAGCAGGATGCACAGGACAGCGCATCTCAGGG  
-----+-----+-----+-----+ 120  
AACGTCTGTGGACCATGGTATGCTTGTCTCGTCTACGTGTCTGTGCGGTAGAGTCCC

b C R T P G T I R T E Q D A Q D S A S Q G -

121 ACTCACCTCTGCCCTGGCGGTGGTTCTTATATTACCAATTGTTGTGGATGTCTGGGCaa  
-----+-----+-----+-----+ 180  
TGAGTGGAGACGGGACCGCCACCAAGAATATAAGTGGTAACAACACCTACAGGACCCGct

b L T S A L A V V L I F T I V V D V L G N -

181 - tatattgggtcattttgtctgtcctgaggaacaagaagctgcagaatgctggaaatctctt  
-----+-----+-----+-----+ 240  
atataaccagtaaaacagacaggactccttgttcttcgacgtcttacgaccttagagaa

b I L V I L S V L R N K K L Q N A G N L F -

241 tgttgtcagtttgtctattgccgatCTGGTTGTTCCTGTGTATCCCTATCCGGTCATTCT  
-----+-----+-----+-----+ 300  
acaacagtcaaacagataaacggctaGACCAACAACGACACATAGGGATAGGCCAGTAAGA

b V V S L S I A D L V V A V Y P Y P V I L -

301 CATAGCTATTTTCCAGAATGGATGGACGCTTGGAAATATCCATTGTCAGATCAGTGGCTT  
-----+-----+-----+-----+ 360  
GTATCGATAAAAGGTCTTACCTACCTGCGAACCTTTATAGGTAACAGTCTAGTCACCGAA

b I A I F Q N G W T L G N I H C Q I S G F -

FIG. 1a

361 CCTGATGGGACTCAGCGTTATTGGATCAGTCTTCAACATAACAGCCATAGCTATCAACAG  
 -----+-----+-----+-----+-----+ 420  
 GGACTACCCCTGAGTCGCAATAACCTAGTCAGAAGTTGTATTGTCGGTATCGATAGTTGTC

b L M G L S V I G S V F N I T A I A I N R -

421 GTATTGCTACATCTGCCACAGCCTGAGATATGACAAGCTTTATAATCAAAGAAGCACCTG  
 -----+-----+-----+-----+-----+ 480  
 CATAACGATGTAGACGGTGTCTGACTCTATACTGTTTCGAAATATTAGTTTCTTCGTGGAC

b Y C Y I C H S L R Y D K L Y N Q R S T W -

481 GTGCTACCTTGGCCTGACATGGATACTAACTATAATTGCAATCGTGCCAAACTTTTTTGT  
 -----+-----+-----+-----+-----+ 540  
 CACGATGGAACCGGACTGTACCTATGATTGATATTAACGTTAGCACGGTTTGAAAAACA

b C Y L G L T W I L T I I A I V P N F F V -

541 TGGATCACTACAGTATGACCCCAGGATTTTTTCTTGACATTTGCGCAGACAGTGAGTTC  
 -----+-----+-----+-----+-----+ 600  
 ACCTAGTGATGTCATACTGGGGTCCTAAAAAAGAACGTGTAAACGCGTCTGTCACTCAAG

b G S L Q Y D P R I F S C T F A Q T V S S -

601 CTCATACACCATAACAGTAGTGGTGGTGCATTTTATAGTCCCTCTTAGTGTTGTGACATT  
 -----+-----+-----+-----+-----+ 660  
 GAGTATGTGGTATTGTCATCACCACCACGTAAATATCAGGGAGAATCACAACACTGTAA

b S Y T I T V V V V H F I V P L S V V T F -

661 CTGTTACTTAAGAATATGGGTTTTAGTGATCCAAGTCAAACACAGAGTTAGACAAGACTT  
 -----+-----+-----+-----+-----+ 720  
 GACAATGAATTCTTATACCCAAAATCACTAGGTTCAGTTTGTGTCCTCAATCTGTTCTGAA

b C Y L R I W V L V I Q V K H R V R Q D F -

FIG. 1b

721 CAAGCAAAAGTTGACACAAACAGACTTGAGAAATTTCTTGACCATGTTTGTGGTCTTTGT  
-----+-----+-----+-----+-----+ 780  
GTTTCGTTTTCAACTGTGTTTGTCTGAAGTCTTTAAAGAACTGGTACAAACACCAGAAACA

b K Q K L T Q T D L R N F L T M F V V F V -

781 ACTTTTTGCAGTTTGCTGGGCCCCCTTAAACTTTATCGGCCTTGCTGTGGCCATTAATCC  
-----+-----+-----+-----+-----+ 840  
TGAAAAACGTCAAACGACCCGGGGAATTTGAAATAGCCGGAACGACACCGGTAATTAGG

b L F A V C W A P L N F I G L A V A I N P -

841 GTTTCATGTGGCACCAAAGATTCCAGAATGGCTGTTTGTTTTAAGCTATTTTCATGGCCTA  
-----+-----+-----+-----+-----+ 900  
CAAAGTACACCGTGGTTTCTAAGGTCTTACCGACAAACAAATTCGATAAAGTACCGGAT

b F H V A P K I P E W L F V L S Y F M A Y -

901 TTTTAACAGTTGTCTCAATGCTGTTATATATGGTGTGCTAAATCAAACTTCCGCAAGGA  
-----+-----+-----+-----+-----+ 960  
AAAATTGTCAACAGAGTTACGACAATATATACCACACGATTTAGTTTTGAAGGCGTTCCT

b F N S C L N A V I Y G V L N Q N F R K E -

961 GTACAAAAGAATACTGATGTCCTTATTGACTCCAAGACTGTTGTTTCTTGACACATCTAG  
-----+-----+-----+-----+-----+ 1020  
CATGTTTTCTTATGACTACAGGAATAACTGAGGTTCTGACAACAAAGAACTGTGTAGATC

b Y K R I L M S L L T P R L L F L D T S R -

1021 AGGAGGAACTGAGGGATTGAAAAGTAAGCCTTCGCCAGCTGTAACCAACAACAATCAAGC  
-----+-----+-----+-----+-----+ 1080  
TCCTCCTTGACTCCCTAACTTTTCATTCCGAAGCGGTGACATTGGTTGTTAGTTTCG

b G G T E G L K S K P S P A V T N N N Q A -

FIG. 1c

1081 AGATATGCTAGGAGAA GCAAGGTCAC TGTGGCTGAGCAGGAGAAATG GTGCGAAAATGGT  
-----+-----+-----+-----+-----+ 1140  
TCTATACGATCCTCTCTG TCCAGTGACACCGACTGCTCTTTTACCACGCTTTTACCA

b D M L G E A R S L W L S R R N G A K M V -

1141 GATCATCATCAGGCCAAGAAAGCACA AATTECAATCATCCATAAATATTC TGGCCTCA  
-----+-----+-----+-----+-----+ 1200  
CTAGTAGTAGTCGGTTC TTTTCGTGTTAACGTTAGTAGTAGTTTATAAGACCGGAGT

b I I I R P R K A Q I A I I H Q I F W P Q -

1261 GAGTTCATGGGCAACATGCCGTCAAGACACA AAGATTACCGGAGAAGAAGATGGCTGCCG  
-----+-----+-----+-----+-----+ 1260  
CTCAAGTACCCGTTGTAC GGCAGTCTGTGTTTCTAATGGCCTCTTCTCTACCGACGGC

b S S W A T C R Q D T K I T G E E D G C R -

1261 TGAAC TGTGCAAGGACGGGATTTC CCAAGGTGAGACCCCAATGCAC TATATCCACATTAT  
-----+-----+-----+-----+-----+ SEQ ID NO: 1  
ACTTGACACGTTCTCTG CCCCCTAAAGGGTTTCCACTCTG GGTACGTGATATAGGTGTAATA  
-----+-----+-----+-----+ 1320

b E L C K D G I S Q R \* SEQ ID NO: 2

FIG. 1d

GGGAGCTCGACGCTCTGGGGATCCACCGGCGCCGGCCCTGCCAGCGCGATGGCGGGGCGG  
 1 -----+-----+-----+-----+-----+-----+-----+ 60  
 CCCTCGAGCTGCGAGACCCCTAGGTGGCCGCGGCCGGGACGGTCGCGCTACCGCCCCGCC

a M A G R -

CTGTGGGGCTCGCCGGGCGGGACCCCCAAGGGCAACGGCAGCAGCGCGCTGCTCAACGTC  
 61 -----+-----+-----+-----+-----+-----+-----+ 120  
 GACACCCCGAGCGGCCCGCCCTGGGGGTTCCCGTTGCCGTCGTCGCGCGACGAGTTGCAG

a L W G S P G G T P K G N G S S A L L N V -

TCGCAGGCGGCGCCCGGCGCCGGGACGGTGTGCGGCCGCGGCCCTCGTGGCTGGCCGCC  
 121 -----+-----+-----+-----+-----+-----+-----+ 180  
 AGCGTCCGCGCGGCCCGGCGCCCTGCCACACGCCGCGCGGGAGCACCGACCGGCGG

a S O A A P G A G D G V R P R P S W L A A -

ACCCTCGCCTCCATCCTCATCTTCACCATCGTGGTGGACATCGTGGGCAACCTCCTGGTG  
 181 -----+-----+-----+-----+-----+-----+-----+ 240  
 TGGGAGCGGAGGTAGGAGTAGAAGTGGTAGCACCACTGTAGCACCCGTTGGAGGACCAC

a T L A S I L T F T I V V D I V G N L L V -

GTCCTGTCCGTGTATCGGAACAAGAAGCTGAGGAACGCAGGGAATGTGTTTGTGGTGAGC  
 241 -----+-----+-----+-----+-----+-----+-----+ 300  
 CAGGACAGGCACATAGCCTTGTTCTTCGACTCCTTGCGTCCCTTACACAAACACCACTCG

a V L S V Y R N K K L R N A G N V F V V S -

CTGGCAGTTGCAGACCTGCTGGTGGCCGTGTATCCGTACCCCTTGGCGCTGGCGTCTATA  
 301 -----+-----+-----+-----+-----+-----+-----+ 360  
 GACCGTCAACGTCTGGACGACCACCGGCACATAGGCATGGGGAACCGCGACCGCAGATAT

a L A V A D L L V A V Y P Y P L A L A S I -

GTTAACAATGGGTGGAGCCTGAGCTCCCTGCATTGCCAACTTAGTGGCTTCCTGATGGGC  
 361 -----+-----+-----+-----+-----+-----+-----+ 420  
 CAATTGTTACCCACCTCGGACTCGAGGGACGTAACGGTTGAATCACCGAAGGACTACCCG

a V N N G W S L S S L H C Q L S G F L M G -

FIG. 2a

TTGAGCGTCATCGGGTCCGTTTTTCAGCATCACGGGAATTGCCATCAACCGCTATTGCTGC  
 421 -----+-----+-----+-----+-----+-----+ 480  
 AACTCGCAGTAGCCCAGGCAAAAGTCGTAGTGCCCTTAACGGTAGTTGGCGATAACGACG  
 a L S V I G S V F S I T G I A I N R Y C C -  
  
 ATCTGCCACAGCCTCAGATACGGCAAGCTGTATAGCGGCACGAATTCCTCTGCTACGTG  
 481 -----+-----+-----+-----+-----+-----+ 540  
 TAGACGGTGTCTGGAGTCTATGCCGTTTCGACATATCGCCGTGCTTAAGGGAGACGATGCAC  
 a I C H S L R Y G K L Y S G T N S L C Y V -  
  
 TTCCTGATCTGGACGCTGACGCTCGTGGCGATCGTGCCCAACCTGTGTGTGGGGACCCCTG  
 541 -----+-----+-----+-----+-----+-----+ 600  
 AAGGACTAGACCTGCGACTGCGAGCACCGCTAGCACGGGTGGACACACACCCCTGGGAC  
 a F L I W T L T L V A I V P N L C V G T L -  
  
 CAGTACGACCCGAGGATCTATTCCCTGTACCTTCACGCAGTCCGTCAGCTCAGCCTACACG  
 601 -----+-----+-----+-----+-----+-----+ 660  
 GTCATGCTGGGCTCCTAGATAAGGACATGGAAGTGCGTCAGGCAGTCGAGTCGGATGTGC  
 a Q Y D P R I Y S C T F T O S V S S A Y T -  
  
 ATCGCCGTGGTGGTGTTCATTTCATAGTTCGGATGCTCGTAGTCGTCTTCTGTTACCTG  
 661 -----+-----+-----+-----+-----+-----+ 720  
 TAGCGGCACCACCACAAGGTAAAGTATCAAGGCTACGAGCATCAGCAGAAGACAATGGAC  
 a I A V V V F H F I V P M L V V V F C Y L -  
  
 AGAATCTGGGCCCTGGTTCTTCAGGTCAGATGGAAGGTGAAACCGGACAACAAACCGAAA  
 721 -----+-----+-----+-----+-----+-----+ 780  
 TCTTAGACCCGGGACCAAGAAGTCCAGTCTACCTTCCACTTTGGCCTGTTGTTTGGCTTT  
 a R I W A L V L Q V R W K V K P D N K P K -  
  
 CTGAAGCCCCAGGACTTCAGGAATTTTGTACCATGTTTGTGGTTTTTGTCTCTTTGCC  
 781 -----+-----+-----+-----+-----+-----+ 840  
 GACTTCGGGGTCTTGAAGTCCTTAAACAGTGGTACAAACACCAAAAACAGGAGAAACGG  
 a L K P Q D F R N F V T M F V V F V L F A -  
  
 ATTTGCTGGGCTCCTCTGAACCTTCATTGGTCTCGTTGTGGCCTCGGACCCCGCCAGCATG  
 841 -----+-----+-----+-----+-----+-----+ 900  
 TAAAGGACCCGAGGAGACTTGAAGTAACCAGAGCAACACCGGAGCCTGGGGCGGTCTGTAC  
 a I C W A P L N F I G L V V A S D P A S M -

FIG. 2b

GCACCCAGGATCCCCGAGTGGCTGTTTGTGGCTAGTTACTATATGGCATATTTCAACAGC  
 901 -----+-----+-----+-----+-----+ 960  
 CGTGGGTCCTAGGGGCTCACCGACAAACACCGATCAATGATATACCGTATAAAGTTGTCTG  
 a     A P R I P E W L F V A S Y Y M A Y F N S -

TGCCTCAATGCGATCATATATGGACTACTGAACCAAAATTTTCAGGCAGGAATACAGAAAA  
 961 -----+-----+-----+-----+-----+ 1020  
 ACGGAGTTACGCTAGTATATACCTGATGACTTGGTTTTAAAGTCCGTCCTTATGTCTTTT  
 a     C L N A I I Y G L L N Q N F R Q E Y R K -

ATTATAGTCTCATTGTGTACCACCAAGATGTTCTTTGTGGATAGCTCCAATCATGTAGCA  
 1021 -----+-----+-----+-----+-----+ 1080  
 TAATATCAGAGTAACACATGGTGGTTCTACAAGAAACACCTATCGAGGTTAGTACATCGT  
 a     I I V S L C T T K M F F V D S S N H V A -

GATAGAATTAAACGCAAACCCTCTCCATTAATAGCCAACCATAACCTAATAAAGGTGGAC  
 1081 -----+-----+-----+-----+-----+ 1140  
 CTATCTTAATTTGCGTTTGGGAGAGGTAATTATCGGTTGGTATTGGATTATTTCCACCTG  
 a     D R I K R K P S P L I A N H N L I K V D -

TCCGTTTAA SEQ ID NO:3  
 1141 ----- 1149  
 AGGCAAATT  
 a     S V \* - SEQ ID NO:4

FIG. 2c

1 ATGAAGGGCAATGTCAGCGAGCTGCTCAATGCCACTCAGCAGGCTCCAGGCGGCGGGGAG 60  
 -----+-----+-----+-----+-----+  
 TACTTCCCGTTACAGTCGCTCGACGAGTTACGGTGAGTCGTCCGAGGTCCGCCGCCCTC  
 a M K G N V S E L L N A T Q Q A P G G G E -  
  
 61 GGAGGGAGACCACGACCGTCCTGGATGGCCTCTACACTGGCCTTCATCCTCATCTTTACC 120  
 -----+-----+-----+-----+-----+  
 CCTCCCTCTGGTGCTGGCAGGACCTACCGGAGATGTGACCGGAAGTAGGAGTAGAAATGG  
 a G G R P R P S W M A S T L A F I L I F T -  
  
 121 ATCGTGGTGGACATTCTGGGCAACCTGCTGCTCATCCTGTCTGTGTACCGCAACAAGAAG 180  
 -----+-----+-----+-----+-----+  
 TAGCACCACCTGTAAGACCCGTTGGACGACCAGTAGGACAGACACATGGCGTTGTTCTTC  
 a I V V D I L G N L L V I L S V Y R N K K -  
  
 181 CTCACGAACCTCAGGGAATATATTTGTGGTGAGTTTAGCTGTGGCAGACCTCGTGGTGGCT 240  
 -----+-----+-----+-----+-----+  
 GAGTCCTTGAGTCCCTTATATAAACACCACTCAAATCGACACCGTCTGGAGCACCACCGA  
 a L R N S G N I F V V S L A V A D L V V A -  
  
 241 CTTTACCCTTATCCCTTGGTGCTGACATCTATCCTTAACAACGGATCGAATCTGGGATAT 300  
 -----+-----+-----+-----+-----+  
 CAAATGGGAATAGGCAACCACGACTGTAGATAGGAATTGTTGCCTACCTTAGACCCTATA  
 a V Y P Y P L V L T S I L N N G W N L G Y -  
  
 301 CTACACTGTCAACTCAGCGCATTTCTAATGGGCTTGACTGTATCGGCTCGATATTGAAC 360  
 -----+-----+-----+-----+-----+  
 GATGTGACAGTTCAGTCGCGTAAAGATTACCCGAACCTCACAGTAGCCGAGCTATAACTTG  
 a L H C Q V S A F L M G L S V I G S I L N -  
  
 361 ATCACGGCGATCGCTATGAACCGTTACTGCTACATTTGCCACAGCCTCAAGTACGACAAA 420  
 -----+-----+-----+-----+-----+  
 TAGTCCCCCTAGCGATACTTGGCAATGACCATGTAAACGGTGTCGGAGTTCATGCTOTTT  
 a I T G I A M N R Y C Y I C H S L K Y D K -  
  
 421 ATATACAGTAACAAGAACTCGCTCTGCTACGTGTTTCCTCATATGGATGCTGACACTCATC 480  
 -----+-----+-----+-----+-----+  
 TATATGTCATTGTTCTTGAGCGAGACGATGCACAAGGACTATACCTACCACTGTGAGTAG  
 a I Y S N K N S L C Y V F L I W M L T L I -

FIG. 3a



481 GCCATCATGCCCAACCTGCAAACCGGAACACTCCAGTACGATCCCCGGATCTACTCCTGT  
 -----+-----+-----+-----+-----+-----+-----+ 540  
 CGGTAGTACGGGTTGACGTTTGGCCTTGTGAGGTCATGCTAGGGCCCTAGATGAGGACA  
 a A I M P N L Q T G T L Q Y D P R I Y S C -  
 541 ACCTTCACCCAGTCTGTCTAGCTCAGCGTACACGATAGCAGTGGTGGTMTTCATTTCATC  
 -----+-----+-----+-----+-----+-----+-----+ 600  
 TGGAAGTGGGTCAGACAGTTCGAGTCGCATGTGCTATCGTCACCACCAAACGTAAGTAG  
 a T F T Q S V S S A Y T I A V V V F H F I -  
 601 GTGCCTATGATTATTGTCTCTCTGCTACTTAAGGATATGGGTCCTGGTCTTCAGGTC  
 -----+-----+-----+-----+-----+-----+-----+ 660  
 CACGGATACTAATAACAGTAGAAGACGATGAATTCCTATACCCAGGACCAGGAAGTCCAG  
 a V P M I I V I F C Y L R I W V L V L Q V -  
 661 AGACGGAGGGTGAAACCCGACAACAAGCCCAAACCTGAAGCCCCAGGACTTCAGGAACCTTT  
 -----+-----+-----+-----+-----+-----+-----+ 720  
 TCTGCCTCCCACTTTGCGCTGTGTTCGGGTTTGACTTCGGGGTCCTGAAGTCCTTGAAA  
 a R R R V K P D N K P K L K P Q D F R N F -  
 721 GTCACCATGTTTCGTAGTTTGTGTACTTTTGGCATTGTGTTGGGCCCCACTCAACCTCATA  
 -----+-----+-----+-----+-----+-----+-----+ 780  
 CAGTGGTACAAGCATCAAAAACATGAAAAACGGTAACAACCCGGGGTCAGTTGGAGTAT  
 a V T M F V V F V L F A I C W A P L N L I -  
 781 GGTCTTATTGTGGCCTCAGACCCTGCCACCATGGTCCCCAGGATCCCAGAGTGGCTGTTC  
 -----+-----+-----+-----+-----+-----+-----+ 840  
 CCAGAATAACACCGGAGTCTGGGACCGTGGTACCAGGGGTCCTAGGGTCTCACCGACAAG  
 a G L I V A S D P A T M V P R I P E W L F -  
 841 GTGGCTAGTTACTACCTGGCGTACTTCAACAGCTGCCTCAACGCAATTATATACGGACTA  
 -----+-----+-----+-----+-----+-----+-----+ 900  
 CACCGATCAATGATGGACCGCATGAAGTTGTGACGGAGTTGCGTTAATATATGCCTGAT  
 a V A S Y Y L A Y F N S C L N A I I Y G L -  
 901 CTGAATCAGAATTTTCAGAAAGGAATACAAAAGATTATTGTCTCGTTGTGCACAGCCAAG  
 -----+-----+-----+-----+-----+-----+-----+ 960  
 GACTTAGTCTTAAAGTCTTTCCTTATGTTTTCTAATAACAGAGCAACACGTGTGGGTTTC  
 a L N Q N F R K E Y K K I I V S L C T A K -

FIG. 3b



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      ggaaacatcttttggtgagcttagcgggtggcagacctggtggtggccatttatccgtac
1  -----+-----+-----+-----+-----+ 60
      cctttgtagaaacaccactcgaatcgccaccgtctggaccaccaccggtaaataggcatg

a  G N I F V V S L A V A D L V V A I Y P Y -

      ccggttggtgctgatgtcgatatttaacaacgggtggaacctgggctatctgcactgccaa
61 -----+-----+-----+-----+-----+ 120
      ggcaaccacgactacagctataaattggtgcccaccttggacccgatagacgtgacggtt

a  P L V L M S I F N N G W N L G Y L H C Q -

      gtcagtgggttcctgatgggcctgagcgtcatcggtccatattcaacatcaccggcatc
121 -----+-----+-----+-----+-----+ 180
      cagtcacccaaggactaccgggactcgcagtagccgaggtataagttgtagtggccgtag

a  V S G F L M G L S V I G S I F N I T G I -
      -
      -

      gccatcaaccgctactGTTACATCTGCCACAGTCTCAAGTGCGACAACTGTACAGCAGC
181 -----+-----+-----+-----+-----+ 240
      cggtagttggcgatgACAATGTAGACGGTGTACAGGTTACGCTGTTTGACATGTCGTCG

a  A I N R Y C Y I C H S L K C D K L Y S S -

      AAGAACTCCCTCTGCTACGTGCTCCTCATATGGCTCCTGACGGCGGCCGTCCTGCCCAAC
241 -----+-----+-----+-----+-----+ 300
      TTCTTGAGGGAGACGATGCACGAGGAGTATACCGAGGACTGCCGCCGGCAGGACGGGTTG

a  K N S L C Y V L L I W L L T A A V L P N -

      CTCGGTCGTGGGACTCTCCAGTACGAGCCGAGGATCTACTCGTGACCTTCGCCCAGTCC
301 -----+-----+-----+-----+-----+ 360
      GAGGCAGCACCCCTGAGAGGTCATGCTCGGCTCCTAGATGAGCACGTGGAAGCGGGTCAGG

a  L R R G T L Q Y E P R I Y S C T F A O S -

      GTCAGCTCCGCCTACACCATCGCCGTGGTGGTTTTCCACTTCCTCGTCCCATGATCATA
361 -----+-----+-----+-----+-----+ 420
      CAGTCGAGGCGGATGTGGTAGCGGCACCACCAAAAGGTGAAGGAGCAGGGGTACTAGTAT

a  V S S A Y T I A V V V F H F L V P M I I -

      GTCATCTTCTGTTACCTGAGAAATATGGATCCTGGTTCTCCAGGTCAGACAGAGGGTGAAA
421 -----+-----+-----+-----+-----+ 480
      CAGTAGAAGACAATGGACTCTTATACCTAGGACCAAGAGGTCCAGTCTGTCTCCCACTTT

a  V † F C Y L R I W I L V L Q V R Q R V K -

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FIG. 4a

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CCTGACCGCAAACCCAAACTGAAACCACACGACTTCAGGAATTTTGTCAACCATGTTTGTG
481 -----+-----+-----+-----+-----+ 540
GGACTGGCGTTTGGGTTTGACTTTGGTGTGCTGAAGTCCTTAAACAGTGGTACAAACAC
a P D R K P K L K P H D F R N F V T M F V -

GTTTTTGTCTTTTGGCCATTTGCTGGGCTCCTCTGAACCTTCATTGGCCTGGCCGTGGCC
541 -----+-----+-----+-----+-----+ 600
CAAAAACAGGAAAAACGGTAAACGACCCGAGGAGACTTGAAGTAACCGGACCGGCACCGG
a V F V L F A I C W A P L N F I G L A V A -

TCTGACCCCGCCAGCATGGTGCCTAGGATCCAGAGTGGCTGTTTGTGGCCAGTTACTAC
601 -----+-----+-----+-----+-----+ 660
AGACTGGGGCGGTCGTACCACGGATCCTAGGGTCTCACCGACAAACACCGGTCAATGATG
a S D P A S M V P R I P E W L F V A S Y Y -

ATGGCGTATTTCAACAGCTGCCTCAATGCCATTATATCGGGCTACTGGAACCAAAATTTTC
661 -----+-----+-----+-----+-----+ 720
TACCGCATAAAGTTGTCGACGGAGTTACGGTAATATAGCCCGATGACCTTGGTTTTAAAG
a M A Y F N S C L N A I I S G Y W N Q N F -

AGGAAGGAATACAGGAGAATTATAGTCTCGCTCGTGACAGCCAGGGTGTTCTTTGTGGAC
721 -----+-----+-----+-----+-----+ 780
TCCTTCCTTATGTCCTCTTAATATCAGAGCGAGCACTGTCGGTCCCACAAGAAACACCTG
a R K E Y R R I I V S L V T A R V F F V D -

AGCTCTAACGACGTGGCCGATAGGGTTAAATGGAAACCGTCTCCACTGATGACCAACAAT
781 -----+-----+-----+-----+-----+ 840
TCGAGATTGCTGCACCGGCTATCCCAATTTACCTTTGGCAGAGGTGACTACTGGTTGTTA
a S S N D V A D R V K W K P S P L M T N N -

AATGTAGTAAAGGTGGACTCCGTTTAA SEQ ID NO:5
841 -----+-----+-----+-----+ 867
TTACATCATTTCCACCTGAGGCAAATT
a N V V K V D S V * - SEQ ID NO:6

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FIG. 4b

1 ATGGCCCTGCGGCCGGGACGCGAACAGGGACCATGCAGGGCAACGGCAGCGCGCTGCCCA  
 -----+-----+-----+-----+-----+-----+ 60  
 TACCGGGACGCCGGCCCTGCGCTTGTCCTGGTACGTCCCGTTGCCGTCGCGGACGGGT

C M Q G N G S A L P N -

61 ACGCCTCCCAGCCCGTGCTCCGCGGGGACGGCGCGCGGCCCTCGTGGCTGGCGTCCGCCC  
 -----+-----+-----+-----+-----+-----+ 120  
 TCGGAGGGTCGGGCACGAGGCGCCCTGCCGCGCGCGGGAGCACCAGCCGAGGCGGG

C A S Q P V L R G D G A R P S W L A S A L -

121 TAGCCTGCGTCCTCATCTTCACCATCGTGGTGGACATCCTGGGCAACCTCCTGGTCATCC  
 -----+-----+-----+-----+-----+-----+ 180  
 ATCGGACGCAGGAGTAGAAGTGGTAGCACCACTGTAGGACCCGTTGGAGGACCAGTAGG

C A C V L I F T I V V D I L G N L L V I L -

181 TGTCGGTGTATCGGAACAAGAAGCTCAGGAACGCaggaaacatcttttggtgagcttag  
 -----+-----+-----+-----+-----+-----+ 240  
 ACAGCCACATAGCCTTGTTCTTCGAGTCCTGCGTcctttgtagaaacaccactcgaatc

C S V Y R N K K L R N A G N I F V V S L A -

241 cgggtggcagacctggtggtggccatttatccgtacccggttggtgctgatgtcgatattta  
 -----+-----+-----+-----+-----+-----+ 300  
 gccaccgtctggaccaccaccggtaaataggcatgggcaaccacgactacagctataaat

C V A D L V V A I Y P Y P L V L M S I F N -

301 acaacgggtggaacctgggctatctgcactgccaaagtcaagggttcctgatgggcctga  
 -----+-----+-----+-----+-----+-----+ 360  
 tgttgcccaccttggaacccgatagacgtgacggttcagtcacccaaggactacccggact

C N G W N L G Y L H C Q V S G F L M G L S -

FIG. 5a

361 gcgtcatcgggtccatattcaacatcaccggcatcgccatcaaccgctactTGCTACATCT  
 -----+-----+-----+-----+-----+ 420  
 cgcagtagccgaggtataagttgtagtggccgtagcggtagttggcgatgACGATGTAGA

C V I G S I F N I T G I A I N R Y C Y I C -

421 GCCACAGTCTCAAGTACGACAAACTGTACAGCAGCAAGAACTCCCTCTGCTACGTGCTCC  
 -----+-----+-----+-----+-----+ 480  
 CGGTGTCAGAGTTCATGCTGTTTGACATGTCGTCGTTCTTGAGGGAGACGATGCACGAGG

C H S L K Y D K L Y S S K N S L C Y V L L -

481 TCATATGGCTCCTGACGCTGGCGGCCGTCCTGCCCAACCTCCGTGCAGGGACTCTCCAGT  
 -----+-----+-----+-----+-----+ 540  
 AGTATACCGAGGACTGCGACCGCCGGCAGGACGGGTTGGAGGCACGTCCCTGAGAGGTCA

C I W L L T L A A V L P N L R A G T L Q Y -

541 ACGACCCGAGGATCTACTCGTGACCTTCGCCCAGTCCGTGAGCTCCGCCTACACCATCG  
 -----+-----+-----+-----+-----+ 600  
 TGCTGGGCTCCTAGATGAGCACGTGGAAGCGGGTCAGGCAGTCGAGGCGGATGTGGTAGC

C D P R I Y S C T F A Q S V S S A Y T I A -

601 CCGTGGTGGTTTTTCCACTTCCTCGTCCCCATGATCATAGTCATCTTCTGTTACCTGAGAA  
 -----+-----+-----+-----+-----+ 660  
 GGCACCACCAAAAGGTGAAGGAGCAGGGGTACTAGTATCAGTAGAAGACAATGGACTCTT

C V V V F H F L V P M I I V I F C Y L R I -

661 TATGGATCCTGGTTCTCCAGGTCAGACAGAGGGTGAAACCTGACCGCAAACCCAAACTGA  
 -----+-----+-----+-----+-----+ 720  
 ATACCTAGGACCAAGAGGTCCAGTCTGTCTCCCACTTTGGACTGGCGTTTGGGTTTGA

C W I L V L Q V R Q R V K P D R K P K L K -

FIG. 5b

```

721  AACCACAGGACTTCAGGAATTTTGTACCATGTTTGTGGTTTTTGTCTCTTTGCCATTT
-----+-----+-----+-----+-----+-----+-----+-----+ 780
      TTGGTGTCTCTGAAGTCCTTAAACAGTGGTACAAACACCAAAACAGGAGAAACGGTAAA

      C   P Q D F R N F V T M F V V F V L F A I C -

      GCTGGGCTCCTCTGAAC TTCATTGGCCTGGCCGTGGCCTCTGACCCCGCCAGCATGGTGC
781  -----+-----+-----+-----+-----+-----+-----+ 840
      CGACCCGAGGAGACTTGAAGTAACCGGACCGGCACCGGAGACTGGGGCGGTCTGTACCACG

      C   W A P L N F I G L A V A S D P A S M V P -

      CTAGGATCCCAGAGTGGCTGTTTGTGGCCAGTTACTACATGGCGTATTTCAACAGCTGCC
841  -----+-----+-----+-----+-----+-----+-----+ 900
      GATCCTAGGGTCTCACC GACAAACACCGGTCAATGATGTACCGCATAAAGTTGTTCGACGG

      C   R I P E W L F V A S Y Y M A Y F N S C L -

      TCAATGCCATTATATACGGGCTACTGAACCAAATTTTCAGGAAGGAATACAGGAGAATTA
901  -----+-----+-----+-----+-----+-----+-----+ 960
      AGTTACGGTAATATATGCCCCGATGACTTGGTTTTAAAGTCCTTCCTTATGTCTCTTAAT

      C   N A I I Y G L L N Q N F R K E Y R R I I -

      TAGTCTCGCTCTGTACAGCCAGGGTGTTCTTTGTGGACAGCTCTAACGACGTGGCCGATA
961  -----+-----+-----+-----+-----+-----+-----+ 1020
      ATCAGAGCGAGACATGTCCGTCCCACAAGAAACACCTGTCGAGATTGCTGCACCGGCTAT

      C   V S L C T A R V F F V D S S N D V A D R -

      GGGTTAAATGGAAACCGTCTCCACTGATGACCAACAATAATGTAGTAAAGGTGGACTCCG
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
      CCCAATTTACCTTTGGCAGAGGTGACTACTGGTTGTTATTACATCATTTCACCTGAGGC

      C   V K W K P S P L M T N N N V V K V D S V -
      (SEQ ID NO:12)

      TTTAA
1081 ----- 1085 (SEQ ID NO:11)
      AAATT

```

FIG. 5c

GGAGAGTCTGCGATGTCAGAGAACGGCTCCTTCGCCAACTGCTGCGAGGCGGGCGGGTGG  
 1 -----+-----+-----+-----+-----+ 60  
 CCTCTCAGACGCTACAGTCTCTTGCCGAGGAAGCGGTTGACGACGCTCCGCCCCCCCACC  
 a M S E N G S F A N C C E A G G W -  
 GCAGTGCGCCCCGGGCTGGTCGGGGGCTGGCAGCGCGCGGCCCTCCAGGACCCCTCGACCT  
 61 -----+-----+-----+-----+-----+ 120  
 CGTCACGCGGGCCCCGACCAGCCCCGACCGTCGCGCGCGCGGGAGGTCCTGGGGAGCTGGA  
 a A V R P G W S G A G S A R P S R T P R P -  
 CCCTGGGTGGCTCCAGCGCTGTCCGCGGTGCTCATCGTCACCACCGCCGTGGACGTCGTG  
 121 -----+-----+-----+-----+-----+ 180  
 GGGACCCACCGAGGTCGCGACAGGCGCCACGAGTAGCAGTGGTGGCGGCACCTGCAGCAC  
 a P W V A P A L S A V L I V T T A V D V V -  
 GGCAACCTCCTGGTGATCCTCTCCGTGCTCAGGAACCGCAAGCTCCGGAACGCAGGTAAT  
 181 -----+-----+-----+-----+-----+ 240  
 CCGTTGGAGGACCACTAGGAGAGGCACGAGTCCTTGGCGTTCGAGGCCTTGCGTCCATTA  
 a G N L L V I L S V L R N R K L R N A G N -  
 TTGTTCTTGGTGAGTCTGGCATTGGCTGACCTGGTGGTGGCCTTCTACCCCTACCCGCTA  
 241 -----+-----+-----+-----+-----+ 300  
 AACCAAGAACCACTCAGACCGTAACCGACTGGACCACCACCGAAGATGGGGATGGGCGAT  
 a L F L V S L A L A D L V V A F Y P Y P L -  
 ATCCTCGTGGCCATCTTCTATGACGGCTGGGCCCCTGGGGGAGGAGCACTGCAAGGCCAGC  
 301 -----+-----+-----+-----+-----+ 360  
 TAGGAGCACCGGTAGAAGATACTGCCGACCCGGGACCCCCCTCCTCGTGACGTTCCGGTCG  
 a I L V A I F Y D G W A L G E E H C K A S -  
 GCCTTTGTGATGGGCCTGAGCGTCATCGGCTCTGTCTTCAATATCACTGCCATCGCCATT  
 361 -----+-----+-----+-----+-----+ 420  
 CGGAAACACTACCCGGACTCGCAGTAGCCGAGACAGAAGTTATAGTGACGGTAGCGGTAA  
 a A F V M G L S V I G S V F N I T A I A I -  
 AACCGCTACTGCTACATCTGCCACAGCATGGCCTACCACCGAATCTACCGGCGCTGGCAC  
 421 -----+-----+-----+-----+-----+ 480  
 TTGGCGATGACGATGTAGACGGTGTCTGACCGGATGGTGGCTTAGATGGCCGCGACCGTG  
 a N R Y C Y I C H S M A Y H R I Y R R W H -

FIG. 6a



481 ACCCCTCTGCACATCTGCCTCATCTGGCTCCTCACCGTGGTGGCCTTGCTGCCCAACTTC 540  
 -----+-----+-----+-----+-----+-----+  
 TGGGGAGACGTGTAGACGGAGTAGACCGAGGAGTGGCACCACCGGAACGACGGGTGAAG  
 a T P L H I C L I W L L T V V A L L P N F -

541 TTTGTGGGGTCCCTGGAGTACGACCCACGCATCTATTCTGACCTTCATCCAGACCGCC 600  
 -----+-----+-----+-----+-----+-----+  
 AAACACCCCAGGGACCTCATGCTGGGTGCGTAGATAAGGACGTGGAAGTAGGTCTGGCGG  
 a F V G S L E Y D P R I Y S C T F I Q T A -

601 AGCACCCAGTACACGGCGGCAGTGGTGGTCATCCACTTCCTCCTCCCTATCGCTGTCTGTG 660  
 -----+-----+-----+-----+-----+-----+  
 TCGTGGGTCTATGTGCCCGCGTCACCACCAGTAGGTGAAGGAGGAGGGATAGCGACAGCAC  
 a S T Q Y T A A V V V I H F L L P I A V V -

661 TCCTTCTGCTACCTGCGCATCTGGGTGCTGGTGCTTCAGGCCCCGAGGAAAGCCAAGCCA 720  
 -----+-----+-----+-----+-----+-----+  
 AGGAAGACGATGGACGCGTAGACCCACGACCACGAAGTCCGGGCGTCCTTTCGGTTCGGT  
 a S F C Y L R I W V L V L Q A R R K A K P -

721 GAGAGCAGGCTGTGCCTGAAGCCCAGCGACTTGCGGAGCTTTCTAACCATGTTTGTGGTG 780  
 -----+-----+-----+-----+-----+-----+  
 CTCTCGTCCGACACGGACTTCGGGTGCTGAACGCCTCGAAAGATTGGTACAAACACCAC  
 a E S R L C L K P S D L R S F L T M F V V -

781 TTTGTGATCTTTGCCATCTGCTGGGCTCCACTTAAGTGCATCGGCCTCGCTGTGGCCATC 840  
 -----+-----+-----+-----+-----+-----+  
 AAACACTAGAAACGGTAGACGACCCGAGGTGAATTGACGTAGCCGGAGCGACACCGGTAG  
 a F V I F A I C W A P L N C I G L A V A I -

841 AACCCCCAAGAAATGGCTCCCCAGATCCCTGAGGGGCTATTTGTCACTAGCTACTTACTG 900  
 -----+-----+-----+-----+-----+-----+  
 TTGGGGGTTCTTTACCGAGGGGTCTAGGGACTCCCCGATAAACAGTGATCGATGAATGAC  
 a N P Q E M A P Q I P E G L F V T S Y L L -

FIG. 6b

```

901  GCTTATTTC AACAGCTGCCTGAATGCCATTGTCTATggtCTTGAACCAAAACTTCCGC
      -----+-----+-----+-----+-----+-----+
      CGAATAAAGTTGTCGACGGACTTACGGTAACAGATACCCGAGAACTTGGTTTGAAGGCG
a    A Y F N S C L N A I V Y G L L N Q N F R -
      960

      AGGGAATACAAGAGGATCCTCTTGGCCCTTTGGAACCCACGGCACTGCATTCAAGATGCT
961  -----+-----+-----+-----+-----+-----+
      TCCCTTATGTTCTCCTAGGAGAACCGGAAACCTTGGGTGCCGTGACGTAAGTTCTACGA
a    R E Y K R I L L A L W N P R H C I Q D A -
      1020

      TCCAAGGGCAGCCACGGAGGGGCTGCAGAGCCCAGCTCCACCCATCATTTGGTGTGCAG
1021 -----+-----+-----+-----+-----+-----+
      AGGTTCCCGTCCGTGGCCTCCCCGACGCTCTCGGGTCGAGGTGGGTAGTAACCAACACGTC
a    S K G S H A E G L Q S P A P P I I G V Q -
      1080

      CACCAGGCAGATGCTCTTAGCCTG (SEQ ID NO:15)
1081 -----+-----+-----+-----+-----+-----+
      GTGGTCCCGTCTACGAGAGATCGGAC
a    H Q A D A L * (SEQ ID NO:16)

```

FIG. 6c

MMEVNSTCLDCRTPGTIRTEQDAQDSASQG.....LT  
MAGRLWGSPPGTPKNGSSALLNVSQAAPGAGDGVPRPWSLA

# I

DO  
JURY

## III

xmr SALAVLIFTIVDVLGNILVLSVLRNKKLQNAQLFVWSLSIADLVAVYPPVILI  
 ov ATLASILFTIVDVLGNLLVLSVYRNKKLRNAGNVFVWSLAVADLLVAVYPYPLALA  
 hum GNIFVWSLAVADLVVAIYPPYPLVLM

huv  
ov  
xuv

### III

xmr	AIFQNGWTLGNIHCQISGFLMGLSVIGSVFNITAI	AINRYCYICHSLRYDKLYNQIRSTW
ov	SIVNNGWSLSSLHCQLSGFLMGLSVIGSVFSITGI	AINRYCCICHSRLRGKLYSGTNSL
hum	SIFNNGWNLGYLHCVQVSGFLMGLSVIGSIFNITGI	AINRYCYICHSLKCDKLYSSKNLSL

hum ov xmr

## IV

xmr CYLGLTWILTIIAIVPNFFVGSQYDPRI FSC TFAQT VSSSYTITWVWHFIVPLSVVT  
 ov CYVFLIWTLTVAIVPNLCVGTQYDPRIYSC TFTQSVSSAYTIAVVFHFIVPMLVVV  
 hum CYVLLIWL LTA .AVLENLRRGTLOVEPRIYSC TFAQSVSSAYTIAVVFHFIVPMIIVI

over 2000

## VI

	Sequence	Accession
xtmr	FCYLRIWVLVIQVKHVRVQDFKQKLQTQDLRNFL	TMFVVFVLFVAVCWAPLNFIGLAVAI
ov	FCYLRIWALVLQVRWKVKPDNKPCLKPQDFRNFV	TMFVVFVLFVAVCWAPLNFIGLVAS
hum	FCYLRIWILVLQVRQVRVKPDRKPKLKPQDFRNFV	TMFVVFVLFVAVCWAPLNFIGLAVAS

100  
 100  
 100

## VII

xmr NPFHVAPKIPFWLSYFMAYFNSCLNAVYGVNLQNFRKEYKRILMSLLTPRLLFLD  
ov DPASMAPRIPEWLFVASYMAYFNSCLNAIYGLNLQNFRQYRKIIVSLCTTKMFFVD  
hum DPASMVPRIPEWLFVASYMAYFNSCLNAIISGYWNQNFRKEYRRIIVSLVTARVFFVD

ov  
xmr  
hum

	TSRGGTEGLKSKPSPAVTNNQADMLGEARSLWLSRRNGAKMVIIRPKAQIAIIHQIF	SEQ ID NO:4
xmr		
ov	SSNHVADRIKRKPSPLIANHNLIKVDSV*	SEQ ID NO:6
hum	SSNDVARDVKWKPSPLMTNNVVKVDSV*	

over  
time

WPOSSWATCRQDTKITGEEDGCRELCKDGISQR

SEQ ID NO:2

FIG. 7

Sheep MAGRLWGSPGGTPKNGSSALLNVSQAAPGAGDGVRRPSPWLAATLASILIFTIVDDIVGNLLVVLVSVYRNKKLRNAGN 79  
 Human MQNGSALPNASQPVLRGDGA...RPSWLASALACVLIFTIVDDILGNLLVILSVYRNKKLRNAGN 63  
 Xenopus MMEVNSTCLDCRTPGTIRTEQDAQDSASQG.....LTSALAWVLIFTIVDDVLGNILVILSVLRNKKLQNAGN 68  
 Consensus -----L-----L-----LIFTIVDD--GN-LV-LSV-RNKKL-NAGN

II  
 Sheep VFWSLAVADLLVAVYPYPLALASIVNNGWSLSSLHCQLSGFLMGLSVIGSVFSITGIAINRYCCICHSLRYGKLYSGT 158  
 Human IFVWSLAVADLVVAIYPYPLVLMISIFNNGWNLGYLHCQVSGFLMGLSVIGSFENITGIAINRYCYICHSLKYDKLYSSK 142  
 Xenopus LFVWSLSIADLVVAVYPYPVILIAIFQNGWTLGNHCQISGFLMGLSVIGSVFNITAIINRYCYICHSLRYDKLYNQR 147  
 Consensus -FVWSL--ADL-VA-YPYp--L--I--NGW-L---HCQ-SGFLMGLSVIGS-F-IT-IAINRYC-ICHSL-Y-KLY----

IV  
 Sheep NSLCYVFLIWTLLVAIVPNLCVGTQLQYDPRIYSCFTQSVSSAYTIAVWFHFIVPMLVWFVFCYLRIWALVLQVRWKV 237  
 Human NSLCYVLLIWLTLAAVLPNLRAGTLQYDPRIYSCFQAQSVSSAYTIAVWFHFELVPMIIVIFCYLRIWILVLQVRQRV 221  
 Xenopus STWCYLGLTWILTIIAIVPNFVGSQYDPRIYSCFQAQTVSSSYTITVWVWFHFIVPLSVVTFCYLRIWVLVIQVKHRV 226  
 Consensus ---CY--L-W-LT--A--?N--G-LQYDPRI-SCTF-Q-VSS-YTI-VWV-HF-VP---V-FCYLRIW-LV-QV---V

VII  
 Sheep KPDNKPKLKPQDFRNEVTMFVVFVLFFAICWAPLNFICGLVVASDPASMAPRIPEWLFVASYYMAYFNSCLNAIIYGLLNQ 316  
 Human KPDRKPKLKPQDFRNEVTMFVVFVLFFAICWAPLNFICGLVVASDPASMAPRIPEWLFVASYYMAYFNSCLNAIIYGLLNQ 300  
 Xenopus RQDFKQKLTQTDLRNFLTMEVVFVLFFAVCWAPLNFICGLAVAINPFHVAPKIPWLFVLSYFMAYFNSCLNAVYIGVVLNQ 305  
 Consensus --D-K-KL-P-D-RNF-TMEVVFVLEA-CWAPLNFICGL-VA--P-----P-IPWLFV-SY-MAYFNSCLNA-IYG-LNQ

Sheep NFRQEYRKIIIVSLCTTKMFEVDSSNHVADRIKRPSPLIANHNLIKVDSV 366 (SEQ ID NO:4)  
 Human NFRKEYRRIIVSLCTARVFEVDSSNDVADRVKWKPSPLMTNNNVVKVDSV 350 (SEQ ID NO:12)  
 Xenopus NFRKEYKRILMSLLTPRLLELDTSRGGTEGLKSKPSPAVTNNNQADMLGEARSLWLSRRNGAKWIIIRPRKAQIAIHH 384  
 Consensus NFR-EY--I--SL-T-----F-D-S-----KPSp-----N-N-----

Xenopus QIFWPQSSWATCRQDTKITGEEDGCRELCKDGISQR 420 (SEQ ID NO:2)

FIG. 8



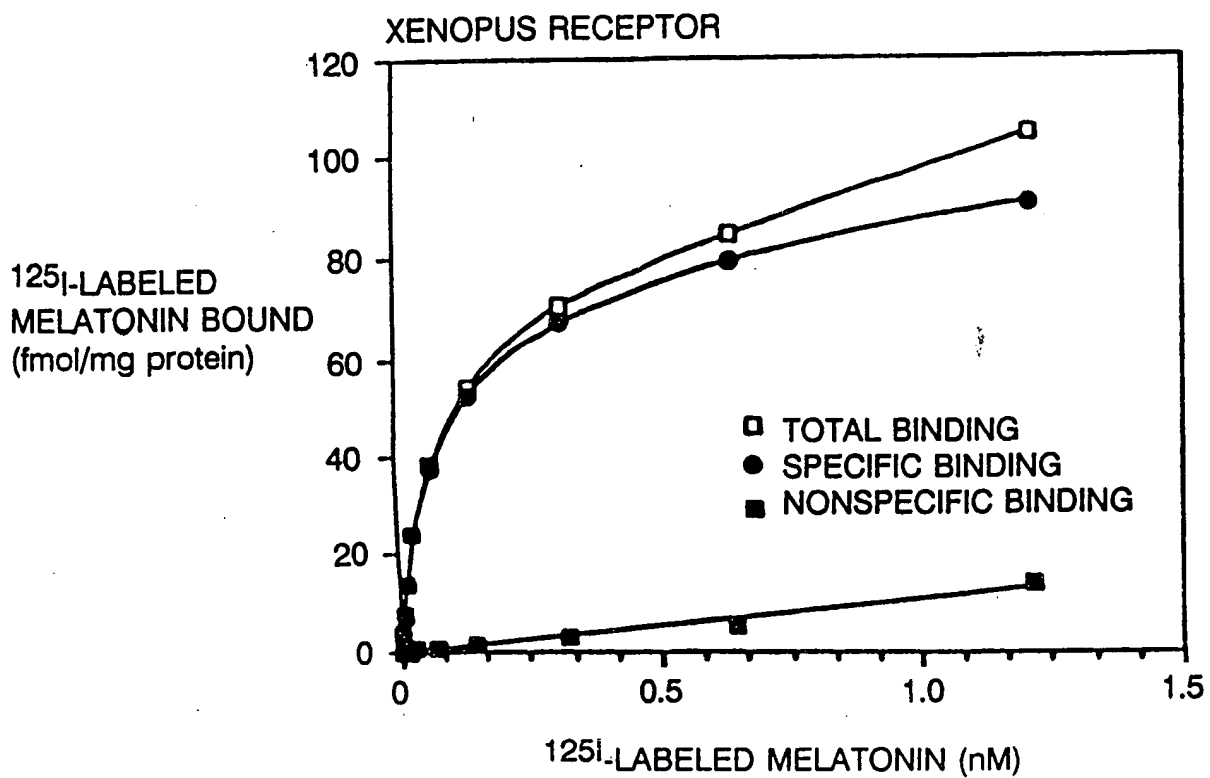


FIG. 10a

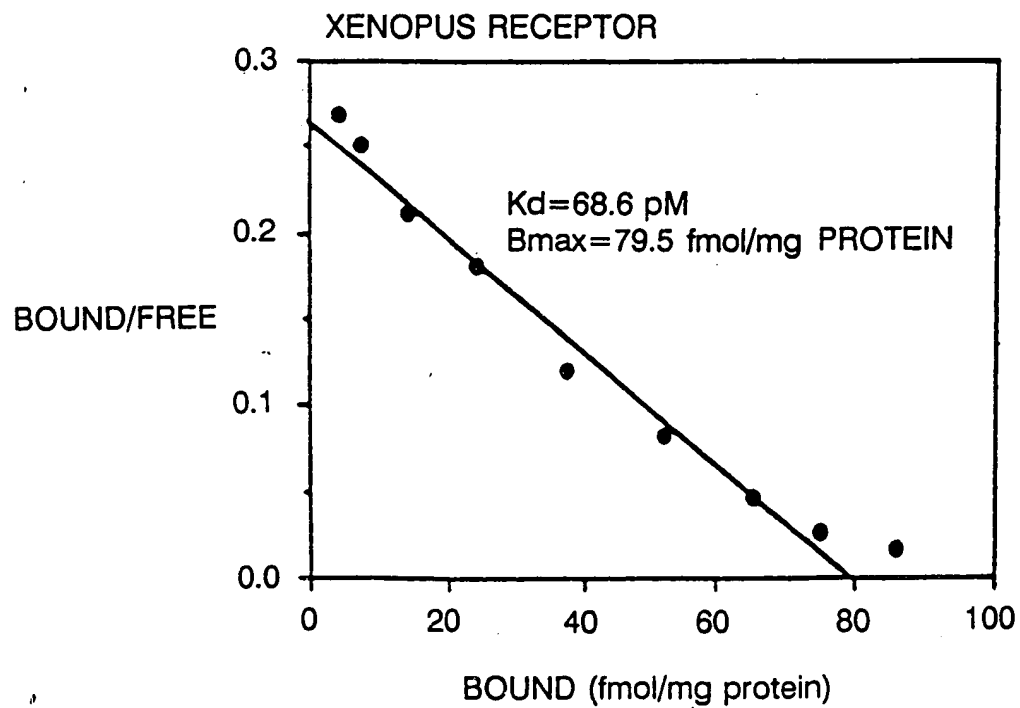


FIG. 10b

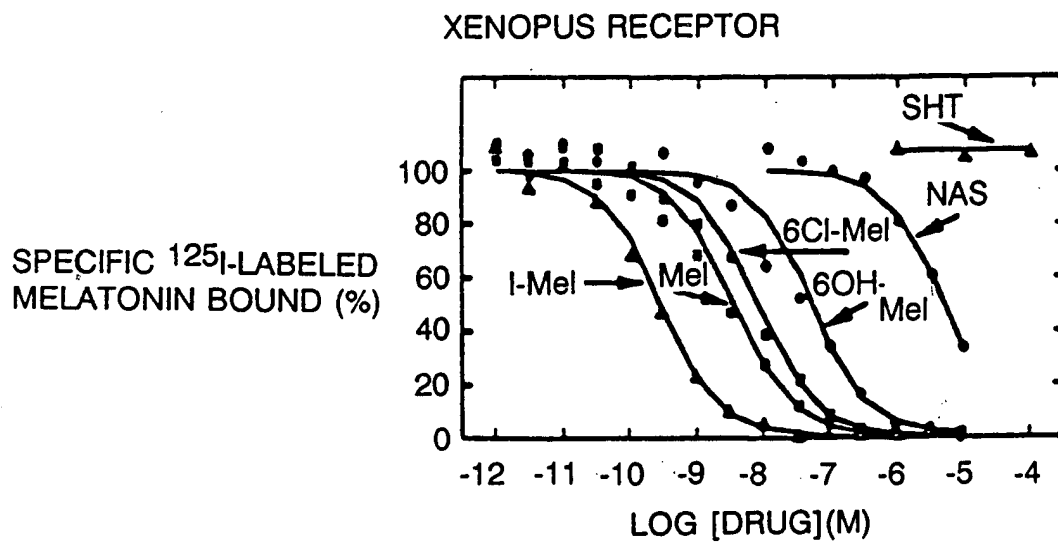


FIG. 11

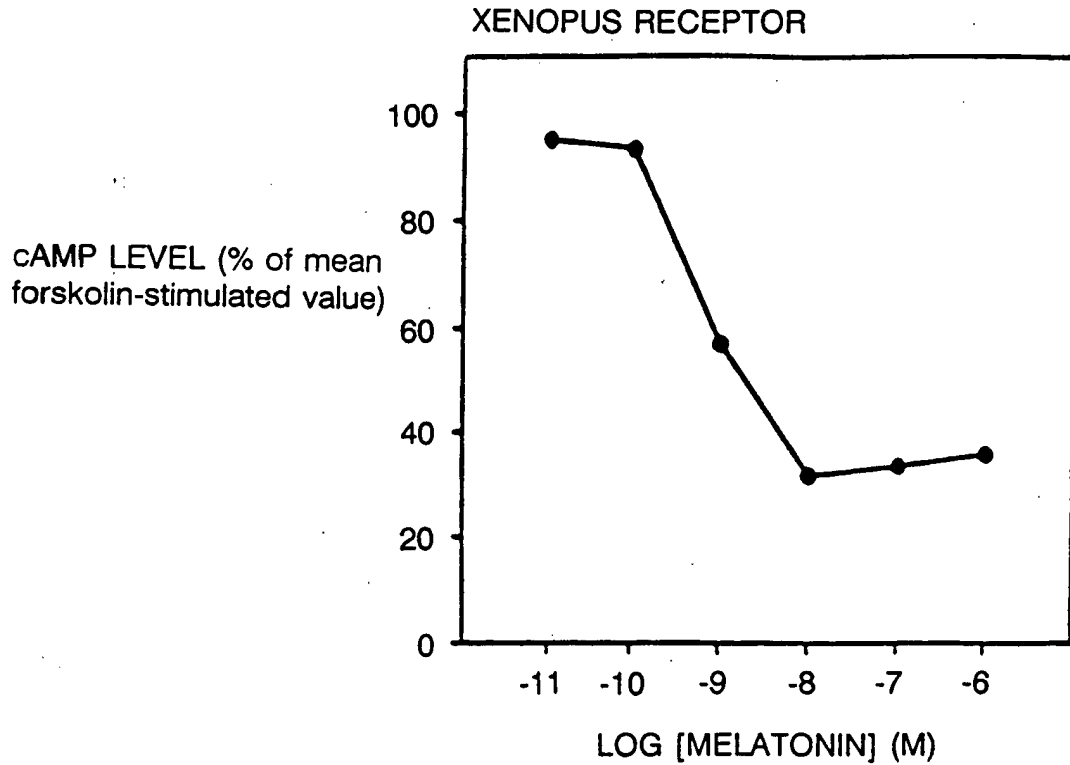


FIG. 12

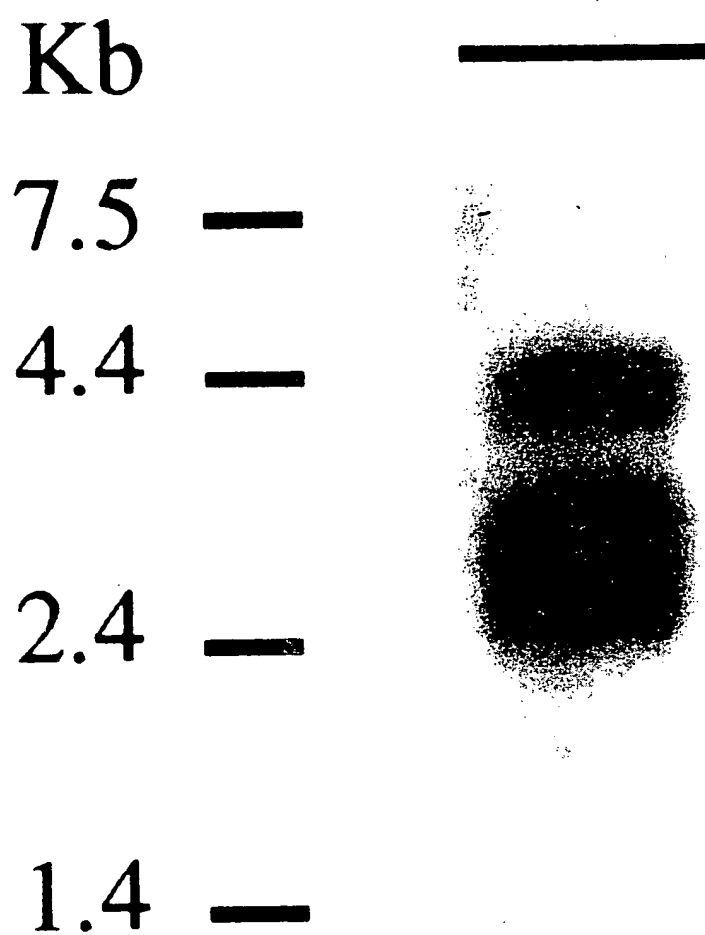


FIG. 13



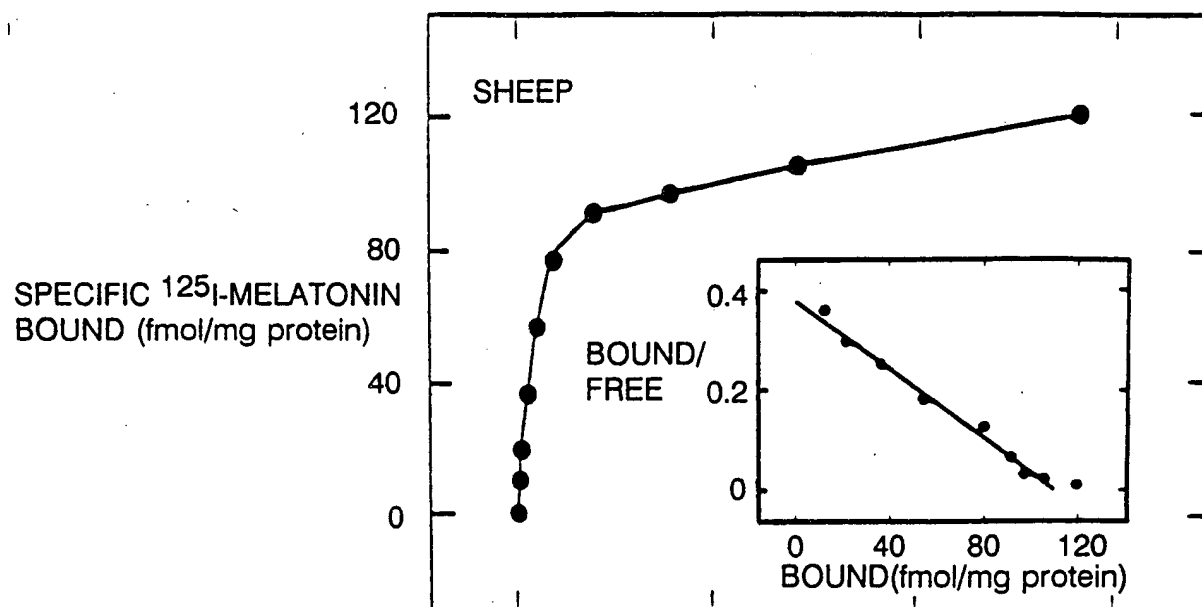


FIG. 14a

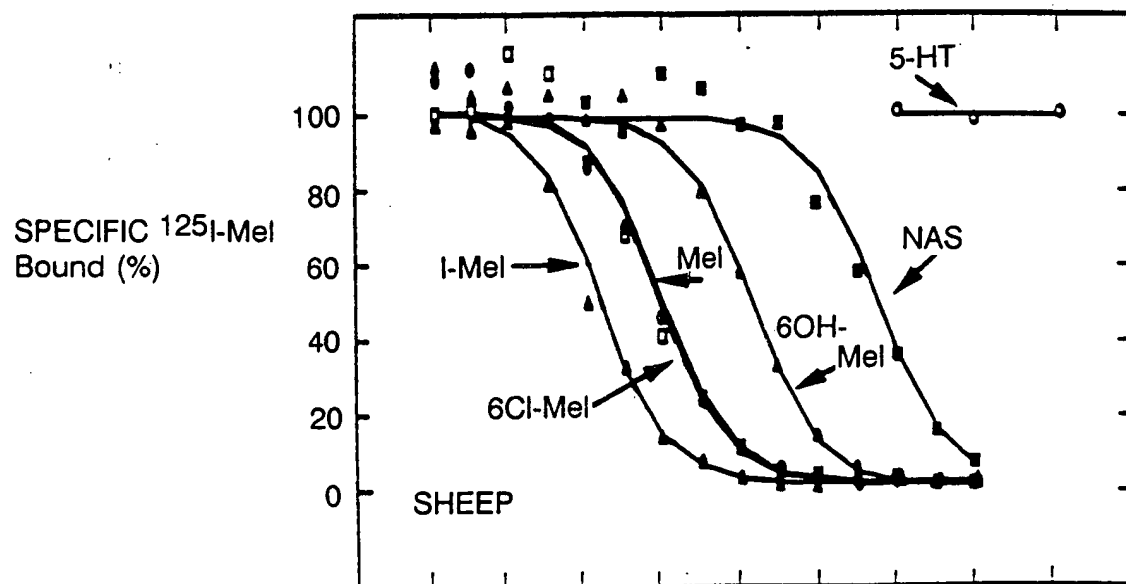


FIG. 14b

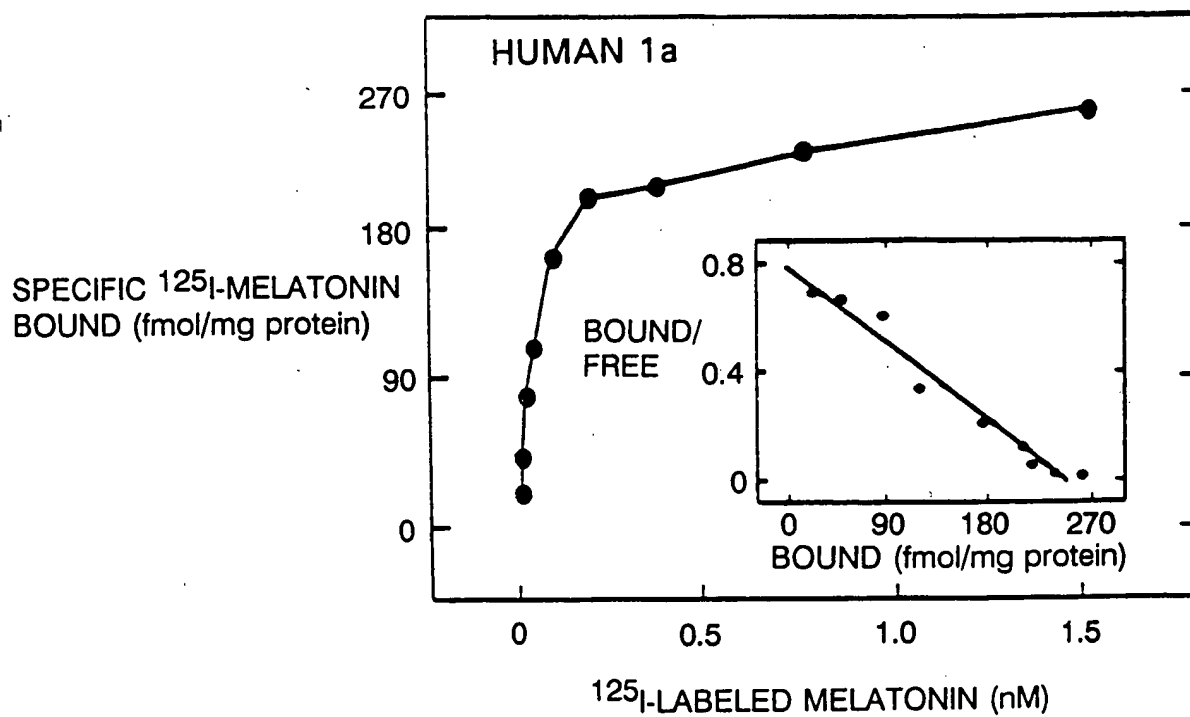


FIG. 15a

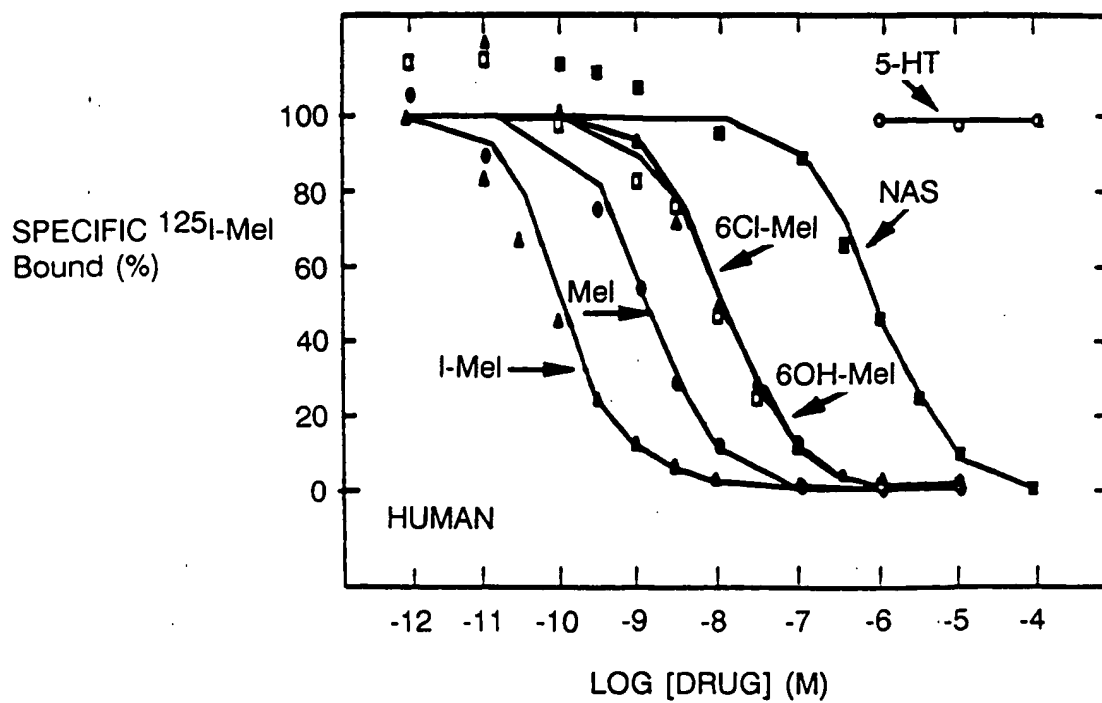


FIG. 15b

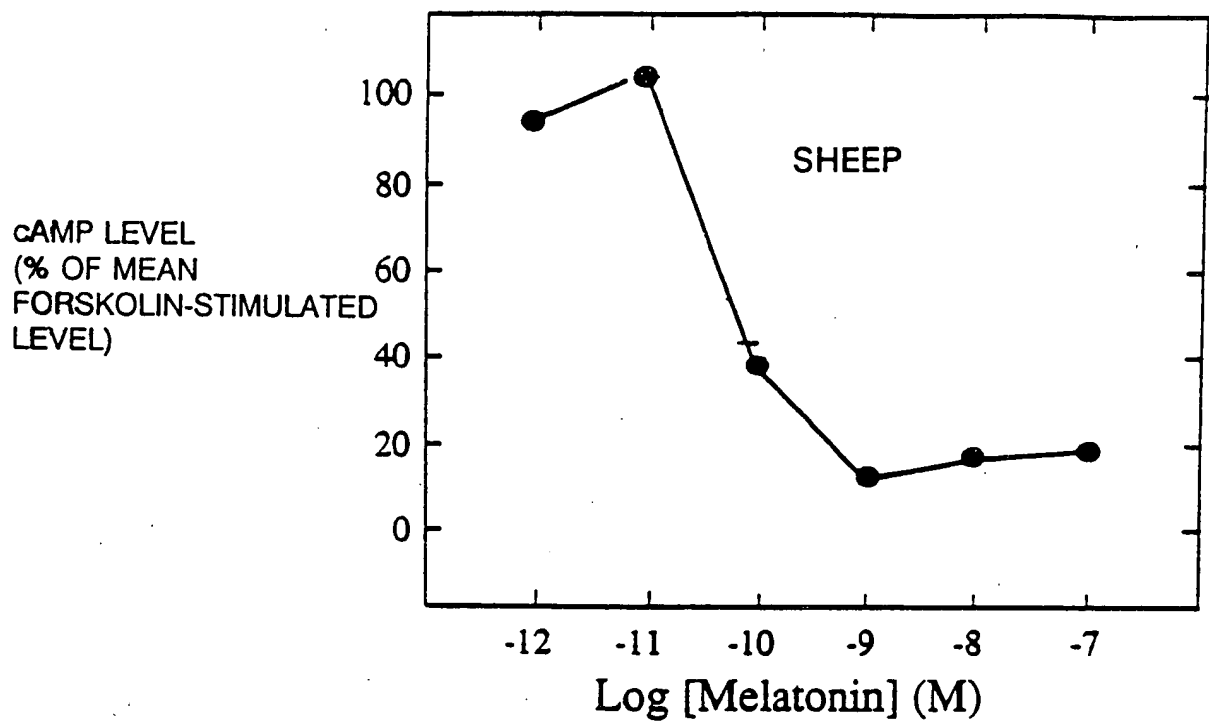


FIG. 16a

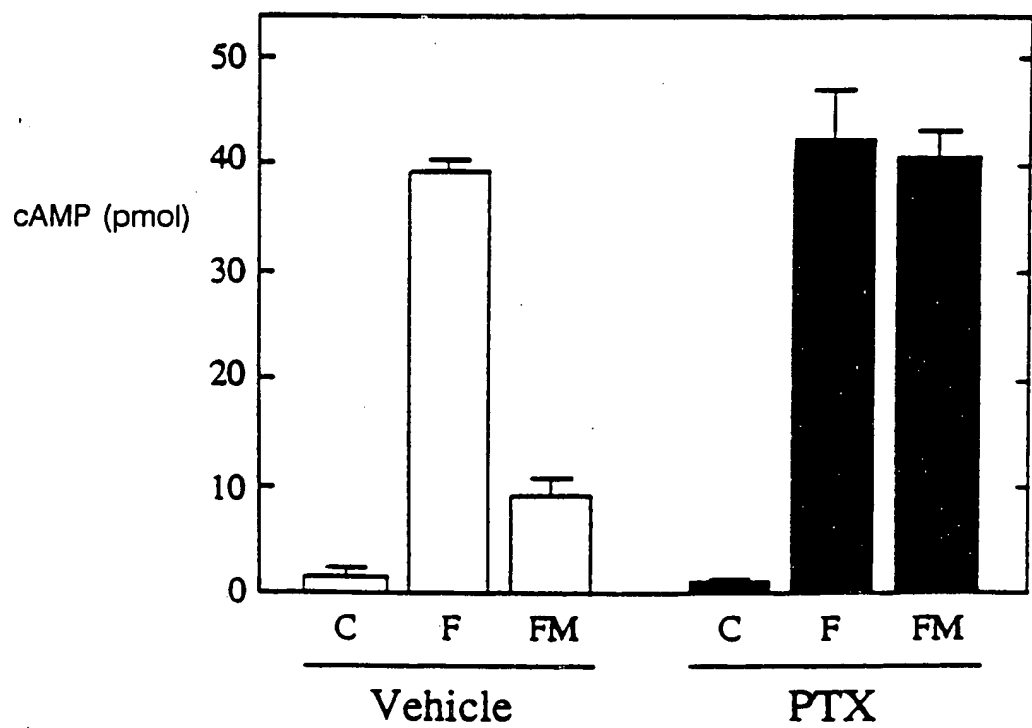
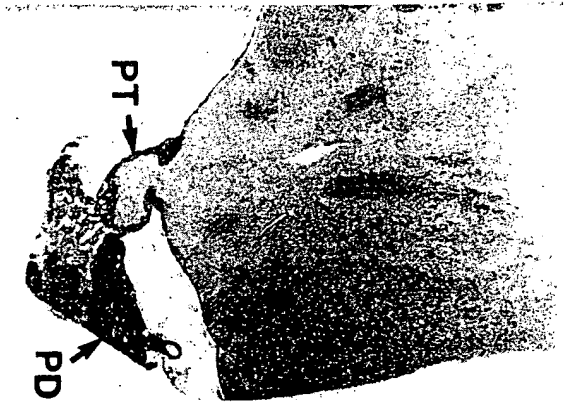


FIG. 16b

**Histology**

**<sup>125</sup>I-MEL Binding**

**mRNA**



**FIG. 17a**



**FIG. 17b**



**FIG. 17c**

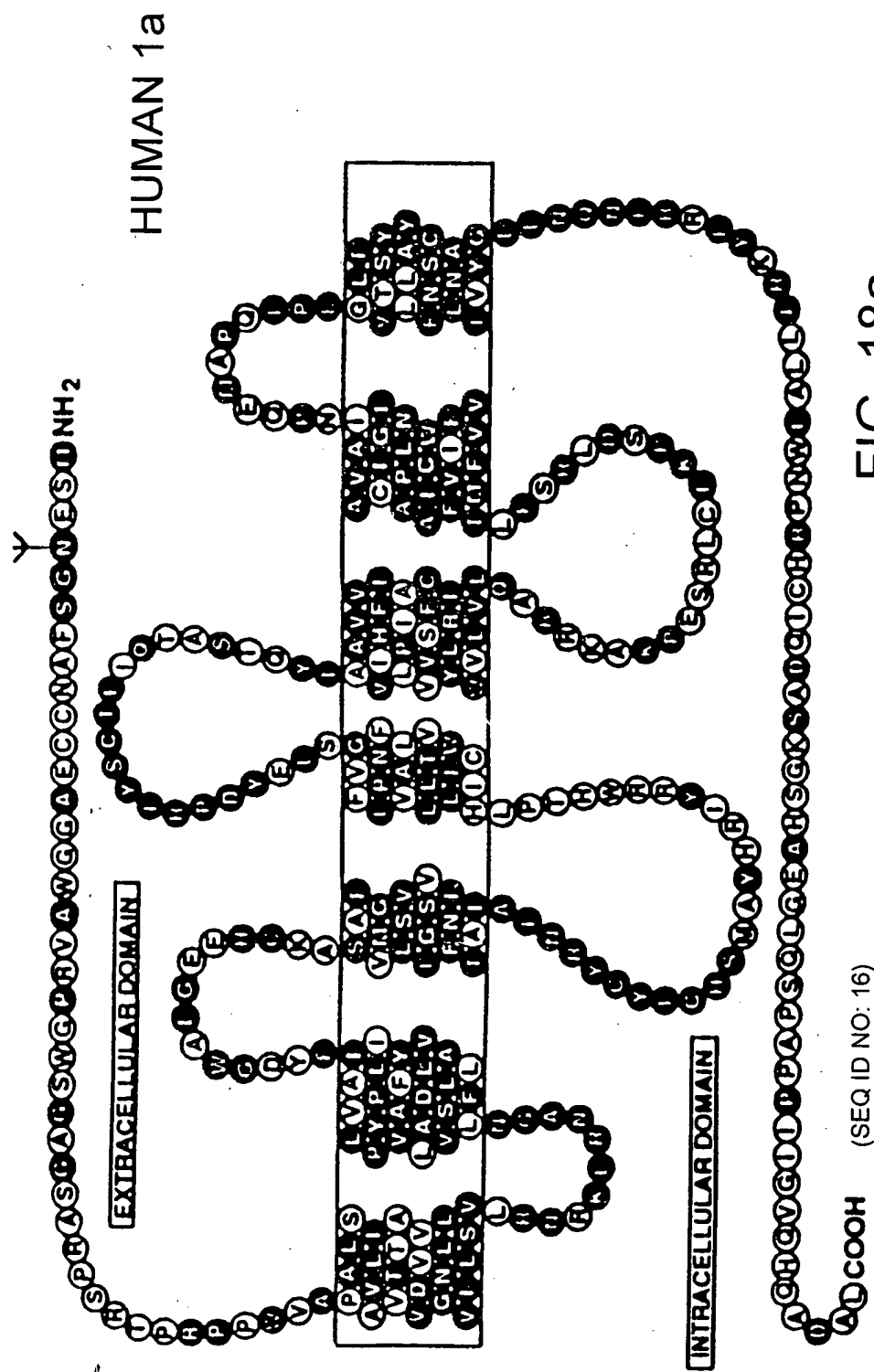


FIG. 18a

Human 1b	<u>I</u>	<u>II</u>
Human 1a	HSNLSFANCCAGGAVRPGSGAGSARSPRPPVAPALSAVLITTTAVDVVGNLLVILSVLRNRKLRNAGNLFVLSLADLLVAFYPPYPLILVAIFYDGHAL	
Xenopus	MQNGSALPNASQPVLRGDCG...RPSWLASALACVLIFTIVVDILGNLLVILSVYRNRKLRNAGNIFVWSLAVADLVVAIYPPYPLVLMHSIFNNGWNL	
Consensus	MMEVNSTCLDCRTPGTIRTEQDAQDSASQG.....LTSALAVVLIFTIVVDVLGNILVILSVLRNKKLQNAGNLFVWLSIADLVVAVYPPYPLILVAFQNGHTL	
	-----AL-VLI-T--VD--GN-LVILSV-RN-KL-NAGN-F-VSL--ADL-VA-YPPY--L--IF--GW-L	
Human 1b	<u>III</u>	<u>IV</u>
Human 1a	GEEHCKASAFVNGLSVIGSVFNITAIAINRYCYICHSHAYHRIYRRWHTPLHICLIWLLTWALLPNFFVGSLEYDPRIYSCTFIQTASTQYTAUVVVIHFLLPVAVVSFC	
Xenopus	GYLHCQVSGFLMGLSVIGSIFNITGIAINRYCYICHSLKCDKLYSSKNSLCYVLLIWLTLAIVLPNLRAGTLQYDPRIYSCTFQSVSSAYTTIAVVFHFLVPMIIVIFC	
Consensus	GNIHCQISGFLMGLSVIGSVFNITAIAINRYCYICHSLRYDKLYNQSTWCYGLTWILTIIAIVPNFFVGSLSQYDPRIESCFAQTVSSSYTITVWVHFIVPLSVVTFC	
	G--HC--S-F-MGLSVIGS-FNIT-IAINRYCYICHS-----Y-----L-W-LT--A--PN--G-L-YDPRI-SCTF-Q--S--YT--VWV-HF--P--V-FC	
Human 1b	<u>VI</u>	<u>VII</u>
Human 1a	YLRIWLVLQARRKAKPESRLCKPDLRSFLTHFVVFVIFAICWAPLNCIGLAVAINPQEMAPQIPEGLFVTSYLLAVFNSCLNAIVYGLLNQNFREYKRILLALNPR	
Xenopus	YLRIWLVLQVRQVRKPDKPKLQDFRNFVTHFVFLFAICWAPLNF IGLAVASDPASHVPRIPFWLFAVSYHAYFNSCLNAIYGLLNQNFREYKRRIIVSLCTAR	
Consensus	YLRIWLVLIQVHRVRQDFKQKLTQTDLRNFLTHTFVTVFLFVAVCWAPLNF IGLAVAINPFHVAPKIPFWLFLSYFMAYFNSCLNAVYGLNQNFRKEYKRILMSLLTPR	
	YLRIW-LV-Q-----L---D-R-F-THFVTVFLFA-CHAPLN-IGLAVA--P-----P-IPE-LFV-SY--AYFNSCLNA--YG-LNQNFREY-RI---L---R	
Human 1b	HCIOASKGSHAEGLOSPAPPIIGVQHQAQDAL 362 (SEQ ID NO:18)	
Human 1a	VFFVDSNDVADRKKPKSPPLMTNNNVKVDV 350 (SEQ ID NO:12)	
Xenopus	LLFLDTSRGGTEGLSKSPSPAVTNNQADMGLGEARSWLSSRRNGAKHVIIIRPKAQIAIIHQIFWPQSSWATCRQDTKITGEEDGCRELCQDGISQR 420	
Consensus	-----D-S-----P-P-----	(SEQ ID NO:2)

FIG. 18b

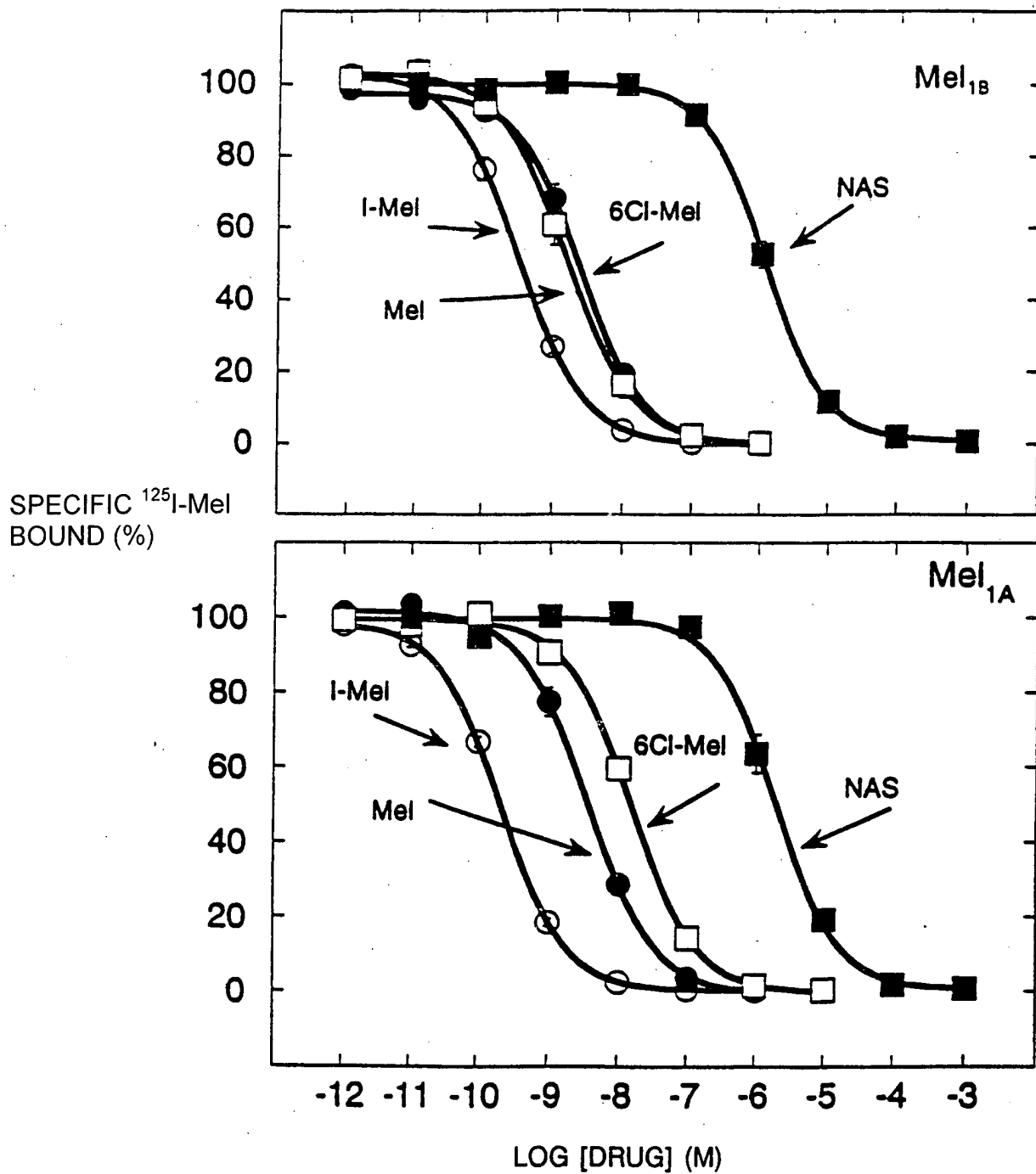


FIG. 20

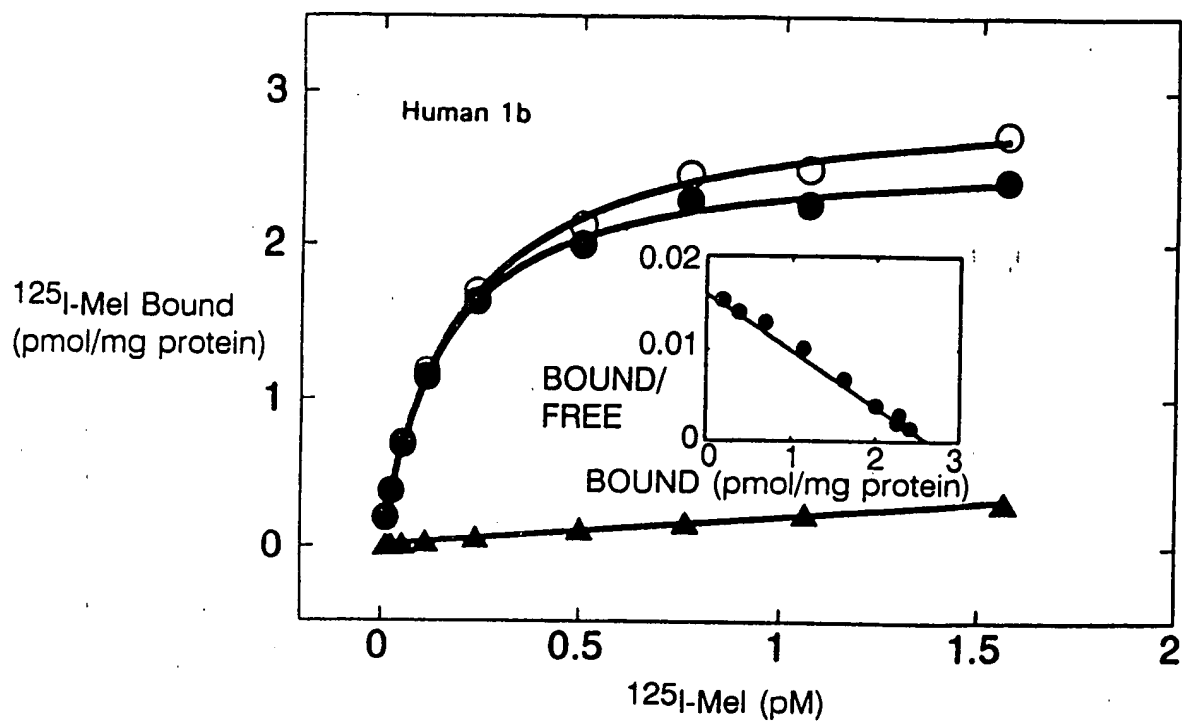


FIG. 19

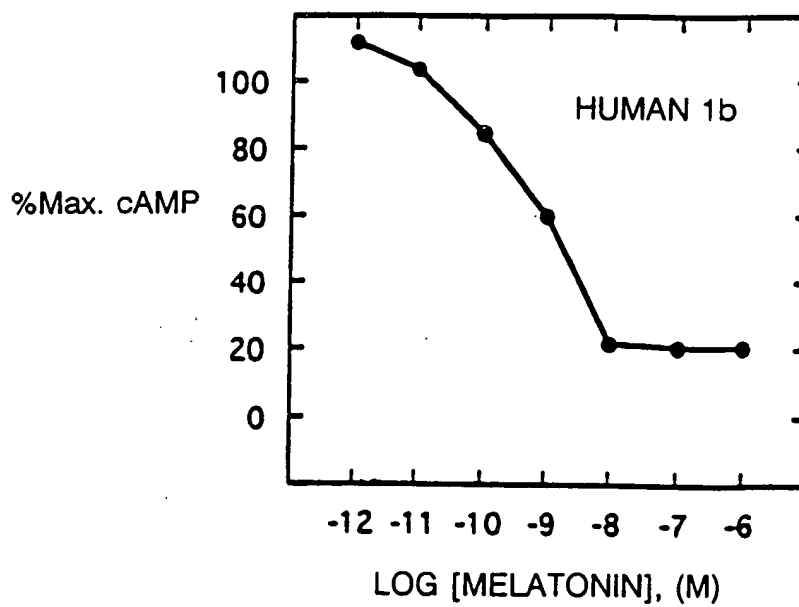


FIG. 21



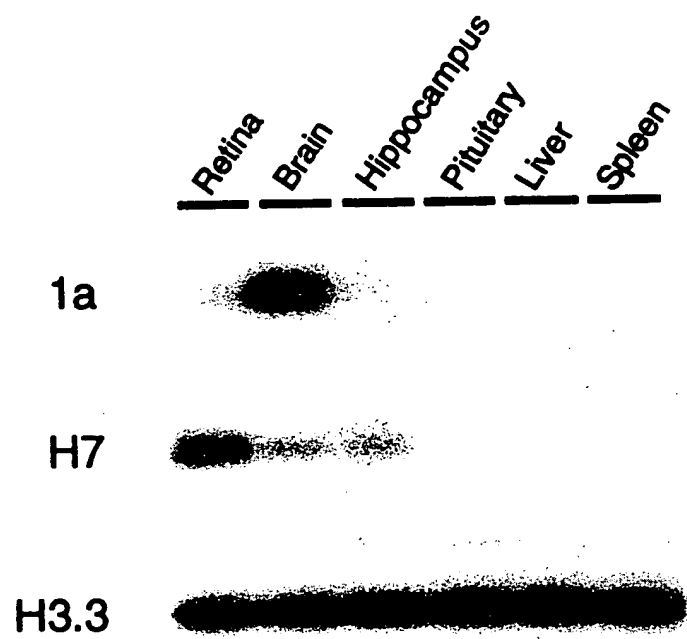


FIG. 22

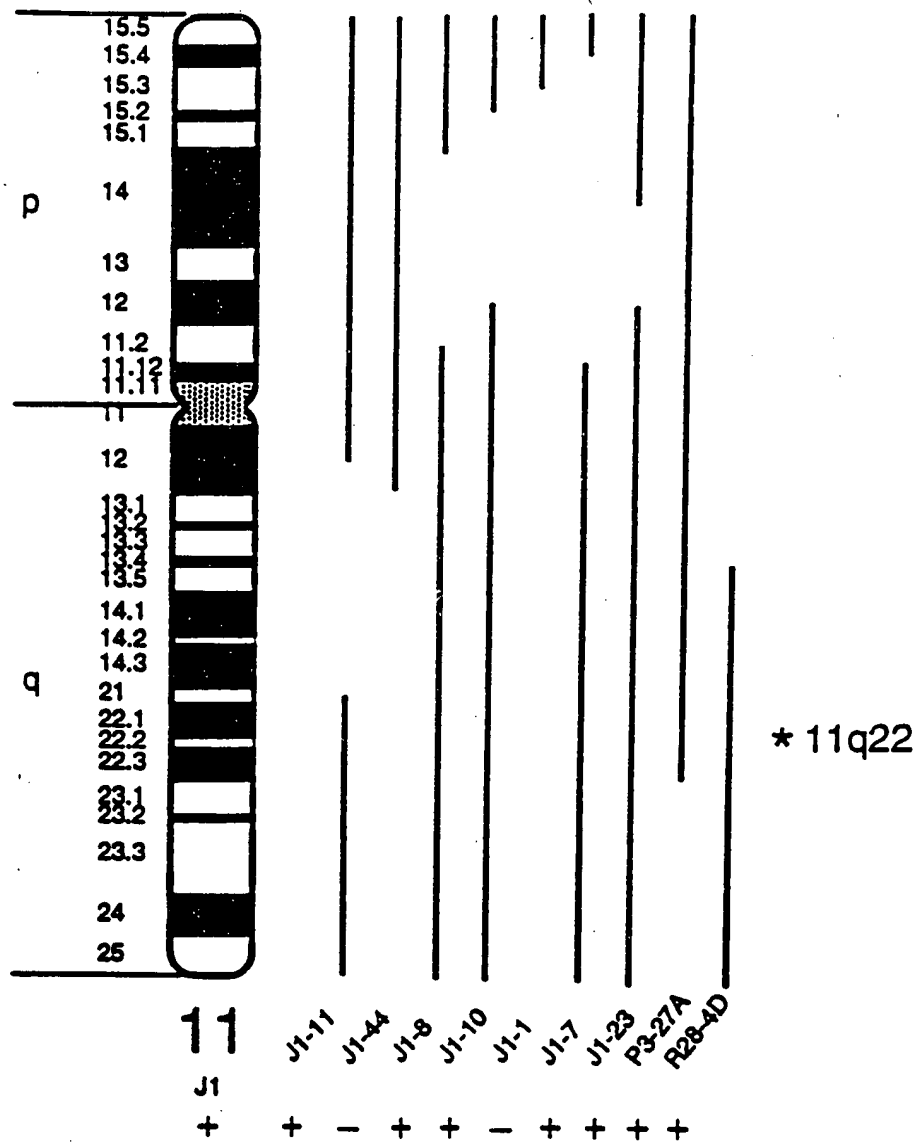


FIG. 23

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